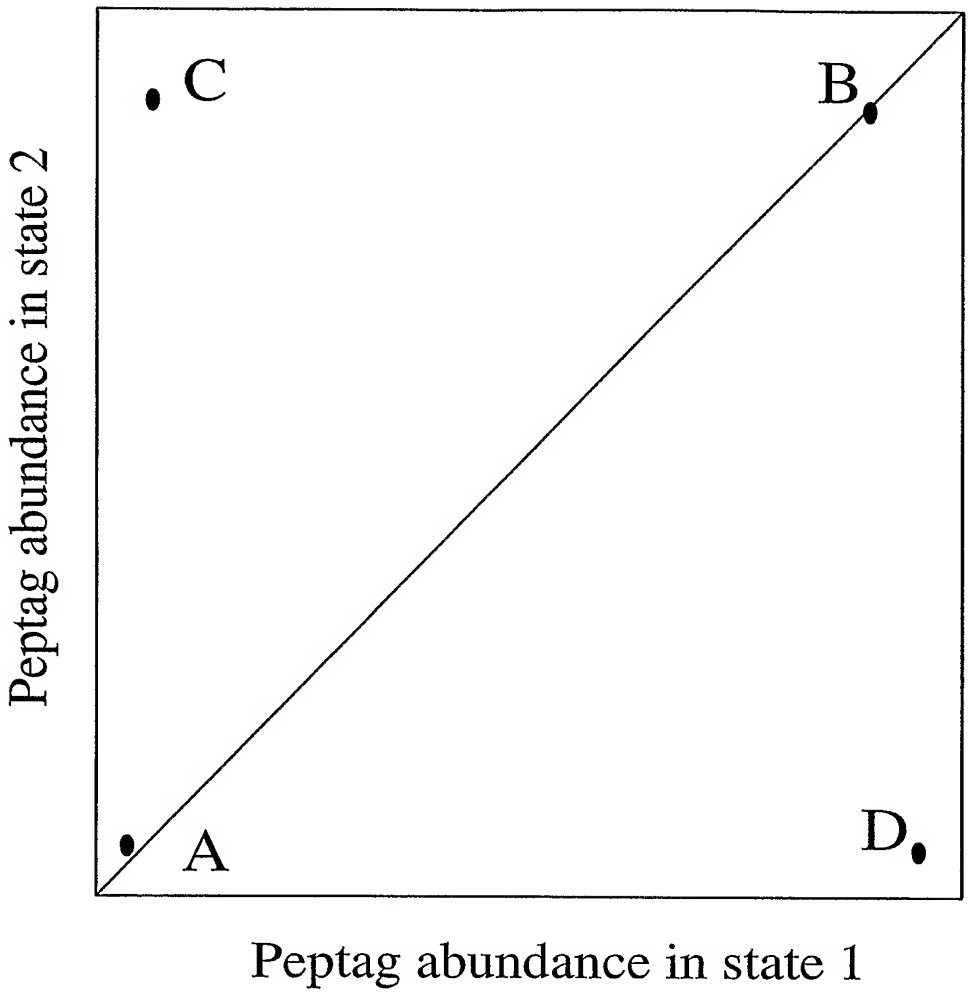
C
B
A
D
Peptag abundance in state 2
Peptag abundance in state 1

FIG. 1

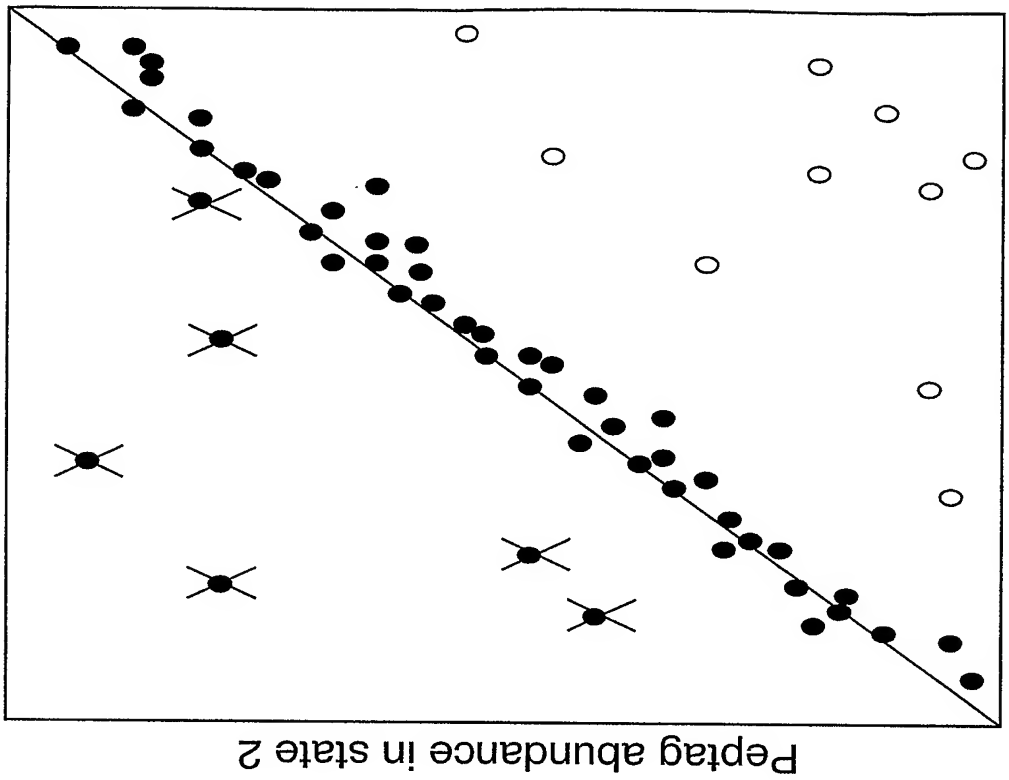
Peptag abundance in state 2
Peptag abundance in state 1

FIG. 2B

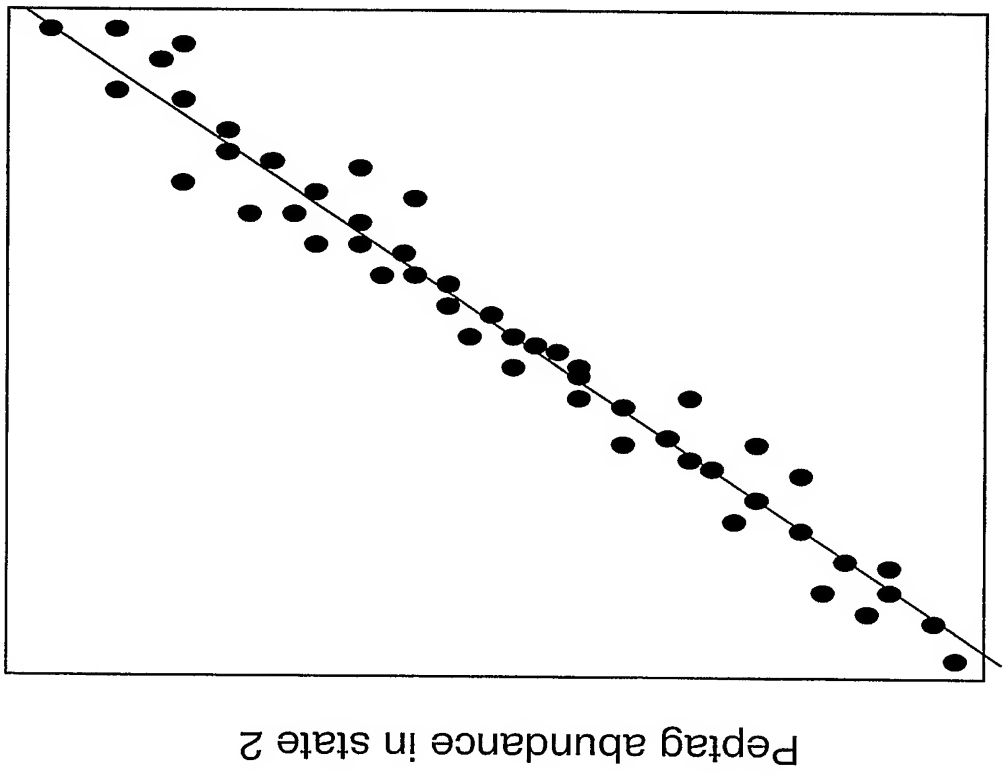
Peptag abundance in state 2
Peptag abundance in state 1

FIG. 2A

Raw automated sequence output from a clone containing a single size-selected concatamer insert using a standard sequencing primer hybridising adjacent to the insert site:

NTNGACTCCTATAGGGCGAATTGGGCCCTCTAGACCCAGATGCAGATCAGAACGAGCAGAGTGAGTCTAGACTCACTCTG

CTGGTTTTCATAGGCATCCTGGTCTAGACCATCAATACGATGAAAACCCGCAGAGTGAGTCTAGACCAAACGCCGGAGTA

AAACTAGCAGAGTGAGTCTAGACTCACTCTGCTCAGTTTCATCGGGTTCCTGGTCTAGACTCACTCTGCTCAGTTTCATC

GTTCGCCTGGTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCAGCACACTGGCGGCCGTT

Annotated sequence output to show the XbaI sites (underlined) that define the junctions between the 37 bp fragments resulting from digestion of the original PCR product. The 21bp variable insert sequences from each phage are shown in bold; this clone contains six ligated fragments:

NTNGACTCCTATAGGGCGAATTGGGCCCTCTAGACC**CAGATGCAGATCAGAACGAGC**AGAGTGAGTCTAGACTCACTCT**G**

CTGGTTTTCATAGGCATCCTGGTCTAGACC**ATCAATACGATGAAAACCCGC**AGAGTGAGTCTAGACC**AAACGCCGGAGTA**

AAACTAGCAGAGTGAGTCTAGACTCACTCT**GCTCAGTTTCATCGGGTTCCT**GGTCTAGACTCACTCT**GCTCAGTTTCATC**

GTTCGCCTGGTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCAGCACACTGGCGGCCGTT

Translation of the 21bp nucleotide sequences into 7-amino acid residue peptide sequences identifies the collective set of peptide sequences capable of binding the target in the original selection experiment:

ARSDLHL
AGFHRHP
AGFHRID
ASFTPAF
AQFHRVP
AQFHRSP

FIG. 3